

REPORTS

Ad1p sequence following Ser²⁰⁸ and occurs within the domain of Ad1p that shows homology with HDE [14]. To delete the complete *STE23* sequence and create the *ste23Δ1-URA3* mutation, polymerase chain reaction (PCR) primers 5'-TCGGAAGACCTCATCTTGCCTCATTTGATATTGCTC-TGTAGATTG-TACTGAGAGTGCAC-3' and 5'-GCTACAAACAGC-GTCAGATGCCGACATCTTCGACTGT-GCGGTATTTCACACCG-3' were used to amplify the *URA3* sequence of pRS316, and the reaction product was transformed into yeast for one-step gene replacement [R. Rothstein, *Methods Enzymol.* 194, 281 (1991)]. To create the *ad1Δ1-LEU2* mutation contained in p114, a 5.0-kb *Sal* I fragment of *pAX1* was cloned into *pLC19*, and an internal 4.0-kb *Hpa* I-*Xba* I fragment was replaced with a *LEU2* fragment. To construct the *ste23Δ1-LEU2* allele (a deletion corresponding to 631 amino acids) carried on p153, a *LEU2* fragment was used to replace the 2.8-kb *Pml* I-*Ecd136* II fragment of *STE23*, which occurs within a 6.2-kb *Hind* II-*Bgl* II genomic fragment carried on pSP72 (Promega). To create *YEpMFA1*, a 1.8-kb *Bam* HI fragment containing *MFA1*, from pKK16 P. Kuchler, R. E. Stern, J. Thomer, *EMBO J.* 8, 3973 (1989), was ligated into the *Bam* HI site of *YEp351* [J. E. Hill, A. M. Myers, T. J. Koerner, A. Tzagoloff, *Yeast* 2, 163 (1986)].

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29. Single-letter abbreviations for the amino acid residues are as follows: A: Ala; C: Cys; D: Asp; E: Glu; F: Phe; G: Gly; H: His; I: Ile; K: Lys; L: Leu; M: Met; N: Asn; P: Pro; Q: Gln; R: Arg; S: Ser; T: Thr; V: Val; W: Trp; and Y: Tyr.

30. A W303 1A derivative, SY2625 (*MATa* *ura3-1* *leu2-3*, *112* *trp1-1* *ade2-1* *can1-100* *ste23Δ1* *mta2Δ1*:*FUS1-1* *his3Δ1*:*FUS1-1**RS2*), was the parent strain for the mutant search. SY2625 derivatives for the mating assays, secreted pheromone assays, and the pulse-chase experiments included the following strains: Y49 (*ste22-1*), Y115 (*mta2Δ1*:*LEU2*), Y142 (*ad1Δ1*:*URA3*), Y173 (*ad1Δ1*:*LEU2*), Y220 (*ad1Δ1*:*URA3* *ste23Δ1*:*URA3*), Y221 (*ste23Δ1*:*URA3*), Y231 (*ad1Δ1*:*LEU2* *ste23Δ1*:*LEU2*), and Y233 (*ste23Δ1*:*LEU2*). *MATa* derivatives of SY2625 included the following strains: Y199 (SY2625 made *MATa*), Y278 (*ste22-1*), Y185 (*mta2Δ1*:*LEU2*), Y196 (*ad1Δ1*:*LEU2*), and Y197 (*ad1Δ1*:*URA3*). The EG123 (*MATa* *leu2* *ura3* *trp1* *can1* *his4*) genetic background was used to create a set of strains for analysis of bud site selection. EG123 derivatives included the following strains: Y175 (*ad1Δ1*:*LEU2*), Y223 (*ad1Δ1*:*URA3*), Y234 (*ste23Δ1*:*LEU2*), and Y272 (*ad1Δ1*:*LEU2* *ste23Δ1*:*LEU2*). *MATa* derivatives of EG123 included the following strains: Y214 (EG123 made *MATa*) and Y293 (*ad1Δ1*:*LEU2*). All strains were generated by means of standard genetic or molecular methods involving the appropriate constructs [23]. In particular, the *ad1* *ste23* double mutant strains were created by crossing of the appropriate *MATa* *ste23* and *MATa* *ad1* mutants, followed by sporulation of the resultant diploid and isolation of the double mutant from nonparental di-type tetrads. Gene disruptions were confirmed with either PCR or Southern (DNA) analysis.
31. p129 is a *YEp352* [J. E. Hill, A. M. Myers, T. J. Koerner, A. Tzagoloff, *Yeast* 2, 163 (1986)] plasmid containing a 5.5-kb *Sal* I fragment of *pAX1*. p151 was derived from p129 by insertion of a linker at the *Bgl* II site within *AX1*, which led to an in-frame insertion of the hemagglutinin (HA) epitope (DQVYDVPDYA) [29] between amino acids B54 and B55 of the *AX1* prod-

uct. pC225 is a *KS+* (Stratagene) plasmid containing a 0.5-kb *Bam* HI-*Sst* I fragment from *pAX1*. Substitution mutations of the proposed active site of Ad1p were created with the use of pC225 and site-specific mutagenesis involving appropriate synthetic oligonucleotides (lex1-*H684*, 5'-GTGCTCACAAAGCGCT-GCCAAACCGGC-3'; *ad1-E71A*, 5'-AAGAACAT-GTGCACAAAGGTGCAC-3'; and *ad1-E71D*, 5'-AAGAACAT-GTGCACAAAGGTGCAC-3'). The mutations were confirmed by sequence analysis. After mutagenesis, the 0.4-kb *Bam* HI-*Msc* I fragment from the mutagenized pC225 plasmids was transferred into *pAX1* to create a set of pRS316 plasmids carrying different *AX1* alleles, p124 (*ad1-H684*), p130 (*ad1-E71A*), and p132 (*ad1-E71D*). Similarly, a set of HA-tagged alleles carried on *YEp352* were created after replacement of the p151 *Bam* HI-*Msc* I fragment, to generate p161 (*ad1-E71A*), p162 (*ad1-*

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Quantitative Monitoring of Gene Expression Patterns with a Complementary DNA Microarray

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A high-capacity system was developed to monitor the expression of many genes in parallel. Microarrays prepared by high-speed robotic printing of complementary DNAs on glass were used for quantitative expression measurements of the corresponding genes. Because of the small format and high density of the arrays, hybridization volumes of 2 microliters could be used that enabled detection of rare transcripts in probe mixtures derived from 2 micrograms of total cellular messenger RNA. Differential expression measurements of 45 *Arabidopsis* genes were made by means of simultaneous, two-color fluorescence hybridization.

The temporal, developmental, topographical, histological, and physiological patterns in which a gene is expressed provide clues to its biological role. The large and expanding database of complementary DNA (cDNA) sequences from many organisms (1) presents the opportunity of defining these patterns at the level of the whole genome.

For these studies, we used the small flowering plant *Arabidopsis thaliana* as a model organism. *Arabidopsis* possesses many advantages for gene expression analysis, including the fact that it has the smallest genome of any higher eukaryote examined to date (2). Forty-five cloned *Arabidopsis* cDNAs (Table 1), including 14 complete sequences and 31 expressed sequence tags (ESTs), were used as gene-specific targets. We obtained the ESTs by selecting cDNA clones at random from an *Arabidopsis* cDNA library. Sequence analysis revealed that 28 of the 31 ESTs matched sequences

in the database (Table 1). Three additional cDNAs from other organisms served as controls in the experiments.

The 48 cDNAs, averaging ~1.0 kb, were amplified with the polymerase chain reaction (PCR) and deposited into individual wells of a 96-well microtiter plate. Each sample was duplicated in two adjacent wells to allow the reproducibility of the arraying and hybridization process to be tested. Samples from the microtiter plate were printed onto glass microscope slides in an area measuring 3.5 mm by 5.5 mm with the use of a high-speed arraying machine (3). The arrays were processed by chemical and heat treatment to attach the DNA sequences to the glass surface and denature them (3). Three arrays, printed in a single lot, were used for the experiments here. A single microtiter plate of PCR products provides sufficient material to print at least 500 arrays.

Fluorescent probes were prepared from total *Arabidopsis* mRNA (4) by a single round of reverse transcription (5). The *Arabidopsis* mRNA was supplemented with human acetylcholine receptor (AChR) mRNA at a dilution of 1:10,000 (w/w) before cDNA synthesis, to provide an internal standard for calibration (5). The resulting fluorescently labeled cDNA mixture was hybridized to an array at high stringency (6) and scanned

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with a laser (3). A high-sensitivity scan gave signals that saturated the detector at nearly all of the *Arabidopsis* target sites (Fig. 1A). Calibration relative to the AChR mRNA standard (Fig. 1A) established a sensitivity limit of $\sim 1:50,000$. No detectable hybridization was observed to either the rat glucocorticoid receptor (Fig. 1A) or the yeast *TRP4* (Fig. 1A) targets even at the highest scanning sensitivity. A moderate-sensitivity scan

of the same array allowed linear detection of the more abundant transcripts (Fig. 1B). Quantitation of both scans revealed a range of expression levels spanning three orders of magnitude for the 45 genes tested (Table 2). RNA blots (7) for several genes (Fig. 2) corroborated the expression levels measured with the microarray to within a factor of 5 (Table 2).

Differential gene expression was investi-

gated with a simultaneous, two-color hybridization scheme, which served to minimize experimental variation inherent in the comparison of independent hybridizations. Fluorescent probes were prepared from two mRNA sources with the use of reverse transcriptase in the presence of fluorescein- and lissamine-labeled nucleotide analogs, respectively (5). The two probes were then mixed together in equal proportions, hybridized to a single array, and scanned separately for fluorescein and lissamine emission after independent excitation of the two fluorophores (3).

To test whether overexpression of a single gene could be detected in a pool of total *Arabidopsis* mRNA, we used a microarray to analyze a transgenic line overexpressing the single transcription factor *HAT4* (8). Fluorescent probes representing mRNA from wild-type and *HAT4*-transgenic plants were labeled with fluorescein and lissamine, respectively; the two probes were then mixed and hybridized to a single array. An intense hybridization signal was observed at the position of the *HAT4* cDNA in the lissamine-specific scan (Fig. 1D), but not in the fluorescein-specific scan of the same array (Fig. 1C). Calibration with AChR mRNA added to the fluorescein and lissamine cDNA synthesis reactions at dilutions of 1:10,000 (Fig. 1C) and 1:100 (Fig. 1D), respectively, revealed a 50-fold elevation of *HAT4* mRNA in the transgenic line relative to its abundance in wild-type plants (Table 2). This magnitude of *HAT4* overexpression matched that inferred from the Northern (RNA) analysis within a factor of 2 (Fig. 2 and Table 2). Expression of all the other genes monitored on the array differed by less than a factor of 5 between *HAT4*-transgenic and wild-type plants (Fig. 1, C

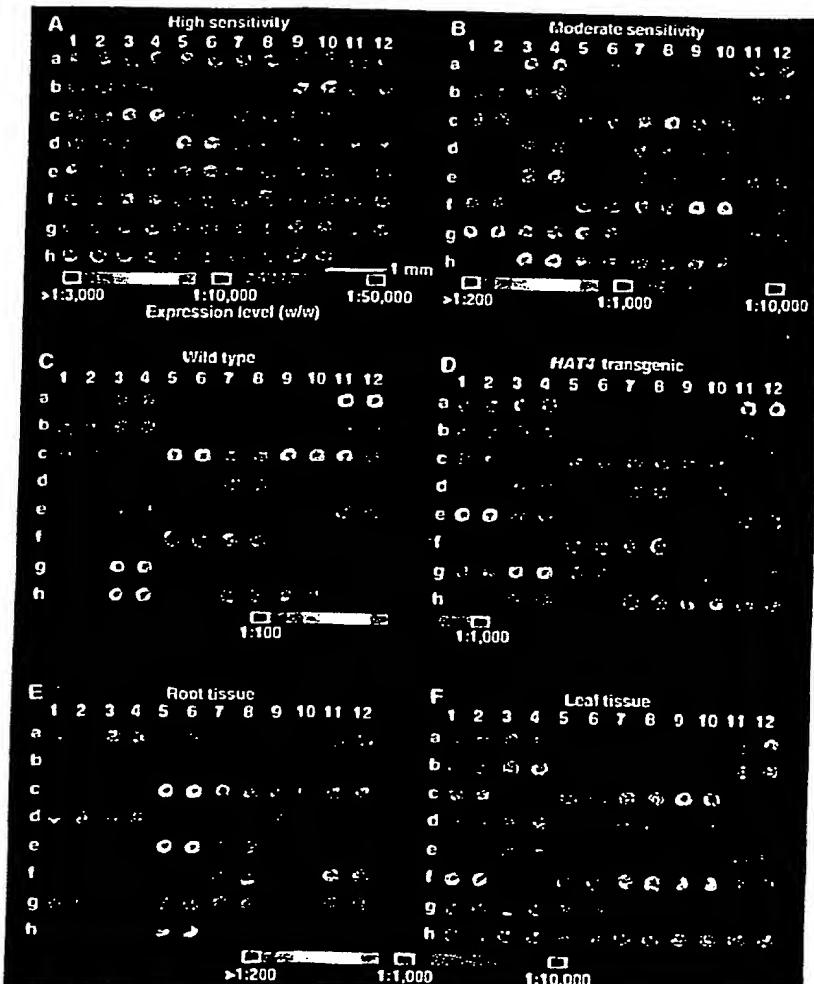


Fig. 1. Gene expression monitored with the use of cDNA microarrays. Fluorescent scans represented in pseudocolor correspond to hybridization intensities. Color bars were calibrated from the signal obtained with the use of known concentrations of human AChR mRNA in independent experiments. Numbers and letters on the axes mark the position of each cDNA. (A) High-sensitivity fluorescein scan after hybridization with fluorescein-labeled cDNA derived from wild-type plants. (B) Same array as in (A) but scanned at moderate sensitivity. (C and D) A single array was probed with a 1:1 mixture of fluorescein-labeled cDNA from wild-type plants and lissamine-labeled cDNA from *HAT4*-transgenic plants. The single array was then scanned successively to detect the fluorescein fluorescence corresponding to mRNA from wild-type plants (C) and the lissamine fluorescence corresponding to mRNA from *HAT4*-transgenic plants (D). (E and F) A single array was probed with a 1:1 mixture of fluorescein-labeled cDNA from root tissue and lissamine-labeled cDNA from leaf tissue. The single array was then scanned successively to detect the fluorescein fluorescence corresponding to mRNAs expressed in roots (E) and the lissamine fluorescence corresponding to mRNAs expressed in leaves (F).

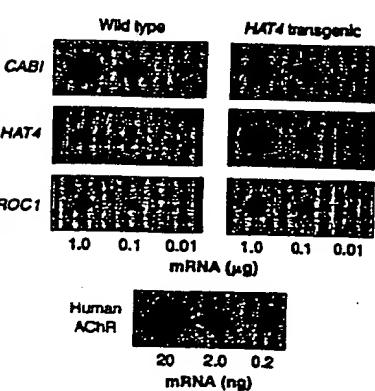


Fig. 2. Gene expression monitored with RNA (Northern) blot analysis. Designated amounts of mRNA from wild-type and *HAT4*-transgenic plants were spotted onto nylon membranes and probed with the cDNAs indicated. Purified human AChR mRNA was used for calibration.

and D, and Table 2). Hybridization of fluorescein-labeled glucocorticoid receptor cDNA (Fig. 1C) and lissamine-labeled TRP4 cDNA (Fig. 1D) verified the presence of the negative control targets and the lack of optical cross talk between the two fluorophores.

To explore a more complex alteration in expression patterns, we performed a second two-color hybridization experiment with fluorescein- and lissamine-labeled probes prepared from root and leaf mRNA, respectively. The scanning sensitivities for the two fluorophores were normalized by matching the signals resulting from AChR

mRNA, which was added to both cDNA synthesis reactions at a dilution of 1:1000 (Fig. 1, E and F). A comparison of the scans revealed widespread differences in gene expression between root and leaf tissue (Fig. 1, E and F). The mRNA from the light-regulated *CAB1* gene was ~500-fold more abundant in leaf (Fig. 1F) than in root tissue (Fig. 1E). The expression of 26 other genes differed between root and leaf tissue by more than a factor of 5 (Fig. 1, E and F).

The *HAT4*-transgenic line we examined has elongated hypocotyls, early flowering, poor germination, and altered pigmentation (8). Although changes in expression were

observed for *HAT4*, large changes in expression were not observed for any of the other 44 genes we examined. This was somewhat surprising, particularly because comparative analysis of leaf and root tissue identified 27 differentially expressed genes. Analysis of an expanded set of genes may be required to identify genes whose expression changes upon *HAT4* overexpression; alternatively, a comparison of mRNA populations from specific tissues of wild-type and *HAT4*-transgenic plants may allow identification of downstream genes.

At the current density of robotic printing, it is feasible to scale up the fabrication process to produce arrays containing 20,000 cDNA targets. At this density, a single array would be sufficient to provide gene-specific targets encompassing nearly the entire repertoire of expressed genes in the *Arabidopsis* genome (2). The availability of 20,274 ESTs from *Arabidopsis* (1, 9) would provide a rich source of templates for such studies.

The estimated 100,000 genes in the human genome (10) exceeds the number of *Arabidopsis* genes by a factor of 5 (2). This modest increase in complexity suggests that similar cDNA microarrays, prepared from the rapidly growing repertoire of human ESTs (1), could be used to determine the expression patterns of tens of thousands of human genes in diverse cell types. Coupling an amplification strategy to the reverse transcription reaction (11) could make it feasible to monitor expression even in minute tissue samples. A wide variety of acute and chronic physiological and pathological conditions might lead to characteristic changes in the patterns of gene expression in peripheral blood cells or other easily sampled tissues. In concert with cDNA microarrays for monitoring complex expression patterns, these tissues might therefore serve as sensitive *in vivo* sensors for clinical diagnosis. Microarrays of cDNAs could thus provide a useful link between human gene sequences and clinical medicine.

Table 1. Sequences contained on the cDNA microarray. Shown is the position, the known or putative function, and the accession number of each cDNA in the microarray (Fig. 1). All but three of the ESTs used in this study matched a sequence in the database. NADH, reduced form of nicotinamide adenine dinucleotide; ATPase, adenosine triphosphatase; GTP, guanosine triphosphate.

Position	cDNA	Function	Accession number
a1, 2	AChR	Human AChR	
a3, 4	EST3	Actin	
a5, 6	EST6	NADH dehydrogenase	H36236
a7, 8	AAC1	Actin 1	227010
a9, 10	EST12	Unknown	M20016
a11, 12	EST13	Actin	U36594†
b1, 2	CAB1	Chlorophyll a/b binding	T45783
b3, 4	EST17	Phosphoglycerate kinase	M85150
b5, 6	G44	Gibberellic acid biosynthesis	T44490
b7, 8	EST19	Unknown	L37126
b9, 10	GBF-1	G-box binding factor 1	U36595†
b11, 12	EST23	Elongation factor	X63894
c1, 2	EST29	Aldolase	X52256
c3, 4	GBF-2	G-box binding factor 2	T04477
c5, 6	EST34	Chloroplast protease	X63895
c7, 8	EST35	Unknown	R87034
c9, 10	EST41	Catalase	T14152
c11, 12	rGR	Rat glucocorticoid receptor	T22720
d1, 2	EST42	Unknown	M14053
d3, 4	EST45	ATPase	U36596†
d5, 6	HAT1	Homeobox-leucine zipper 1	J04185
d7, 8	EST46	Light harvesting complex	U09332
d9, 10	EST49	Unknown	T04063
d11, 12	HAT2	Homeobox-leucine zipper 2	T76267
e1, 2	HAT4	Homeobox-leucine zipper 4	U09335
e3, 4	EST50	Phosphoribulokinase	M90394
e5, 6	HAT5	Homeobox-leucine zipper 5	T04344
e7, 8	EST51	Unknown	M90416
e9, 10	HAT22	Homeobox-leucine zipper 22	Z33675
e11, 12	EST52	Oxygen evolving	U09336
f1, 2	EST59	Unknown	T21749
f3, 4	KNAT1	Knotted-like homeobox 1	Z34607
f5, 6	EST60	RuBisCO small subunit	U14174
f7, 8	EST69	Translation elongation factor	X14564
f9, 10	PPH1	Protein phosphatase 1	T42799
f11, 12	EST70	Unknown	U34803
g1, 2	EST75	Chloroplast protease	T44621
g3, 4	EST78	Unknown	T43698
g5, 6	ROC1	Cyclophilin	R65481
g7, 8	EST82	GTP binding	L14844
g9, 10	EST83	Unknown	X59152
g11, 12	EST84	Unknown	Z33795
h1, 2	EST91	Unknown	T45278
h3, 4	EST96	Unknown	T13832
h5, 6	SAR1	Synaptobrevin	R64816
h7, 8	EST100	Light harvesting complex	M90418
h9, 10	EST103	Light harvesting complex	Z18205
h11, 12	TRP4	Yeast tryptophan biosynthesis	X03909

*Proprietary sequence of Stratagene (La Jolla, California).

†No match in the database; novel EST.

Table 2. Gene expression monitoring by microarray and RNA blot analyses; tg, *HAT4*-transgenic. See Table 1 for additional gene information. Expression levels (w/w) were calibrated with the use of known amounts of human AChR mRNA. Values for the microarray were determined from microarray scans (Fig. 1); values for the RNA blot were determined from RNA blots (Fig. 2).

Gene	Expression level (w/w)	
	Microarray	RNA blot
<i>CAB1</i>	1:48	1:83
<i>CAB1</i> (tg)	1:120	1:150
<i>HAT4</i>	1:8300	1:6300
<i>HAT4</i> (tg)	1:150	1:210
<i>ROC1</i>	1:1200	1:1800
<i>ROC1</i> (tg)	1:260	1:1300

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- The current EST database (dbEST release 091495) from the National Center for Biotechnology Information (Bethesda, MD) contains a total of 322,225 entries, including 255,845 from the human genome and 21,044 from *Arabidopsis*. Access is available via the World Wide Web (<http://www.ncbi.nlm.nih.gov>).
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- D. Shalon, thesis, Stanford University (1995); and P. O. Brown, in preparation. Microarrays were fabricated on poly-L-lysine-coated microscope slides (Sigma) with a custom-built arraying machine fitted with one printing tip. The tip loaded 1 μ l of PCR product (0.5 mg/ml) from 96-well microtiter plates and deposited \sim 0.005 μ l per slide on 40 slides at a spacing of 500 μ m. The printed slides were rehydrated for 2 hours in a humid chamber, snap-dried at 100°C for 1 min, rinsed in 0.1% SDS, and treated with 0.05% succinyl anhydride prepared in buffer consisting of 50% 1-methyl-2-pyrrolidinone and 50% boric acid. The cDNA on the slides was denatured in distilled water for 2 min at 90°C immediately before use. Microarrays were scanned with a laser fluorescent scanner that contained a computer-controlled XY stage and a microscope objective. A mixed gas, multiline laser, allowed sequential excitation of the two fluorophores. Emitted light was split according to wavelength and detected with two photomultiplier tubes. Signals were read into a PC with the use of a 12-bit analog-to-digital board. Additional details of microarray fabrication and use may be obtained by means of e-mail (pbrown@cmgm.stanford.edu).
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- Polyadenylated (poly(A)ⁿ) mRNA was prepared from total RNA with the use of Oligo(dT) resin (Clontech). Reverse transcription (RT) reactions were carried out with a Stratascript RT-PCR kit (Stratagene) modified as follows: 50- μ l reactions contained 0.1 μ g/ μ l of *Arabidopsis* mRNA, 0.1 ng/ μ l of human AChR mRNA, 0.05 μ g/ μ l of oligo(dT) (21-mer), 1X first strand buffer, 0.03 U/ μ l of ribonuclease block, 500 μ M deoxyadenosine triphosphate (dATP), 500 μ M deoxyguanosine triphosphate, 500 μ M dTTP, 40 μ M deoxycytidine triphosphate (dTTP), 40 μ M fluorescein-12-dCTP (or lissamine-5-dCTP), and 0.03 U/ μ l of Stratascript reverse transcriptase. Reactions were incubated for 60 min at 37°C, precipitated with ethanol, and resuspended in 10 μ l of TE (10 mM Tris-HCl and 1 mM EDTA, pH 8.0). Samples were then heated for 3 min at 94°C and chilled on ice. The RNA was degraded by adding 0.25 μ l of 10 N NaOH followed by a 10-min incubation at 37°C. The samples were neutralized by addition of 2.5 μ l of 1 M Tris-HCl (pH 8.0) and 0.25 μ l of 10 N HCl and precipitated with ethanol. Pellets were washed with 70% ethanol, dried to completion in a speedvac, resuspended in 10 μ l of H₂O, and reduced to 3.0 μ l in a speedvac. Fluorescent nucleotide analogs were obtained from New England Nuclear (DuPont).
- Hybridization reactions contained 1.0 μ l of fluorescent cDNA synthesis product (5) and 1.0 μ l of hybridization buffer [10X saline sodium citrate (SSC) and 0.2% SDS]. The 2.0- μ l probe mixtures were aliquoted onto the microarray surface and covered with cover slips (12 mm round). Arrays were transferred to a hybridization chamber (3) and incubated for 18 hours at 65°C. Arrays were washed for 5 min at room temperature (25°C) in low-stringency wash buffer (1X SSC and 0.1% SDS), then for 10 min at room temperature in high-stringency wash buffer (0.1X SSC and 0.1% SDS). Arrays were scanned in 0.1X SSC with the use of a fluorescence laser-scanning device (3).
- Samples of poly(A)ⁿ mRNA (4, 5) were spotted onto nylon membranes (Nytran) and crosslinked with ultraviolet light with the use of a Stratalinker 1800 (Stratagene). Probes were prepared by random priming with the use of a Prime-It II kit (Stratagene) in the presence of ³²PdATP. Hybridizations were carried out according to the instructions of the manufacturer. Quantitation was performed on a PhosphorImager (Molecular Dynamics).
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- The laser fluorescent scanner was designed and fabricated in collaboration with S. Smith of Stanford University. Scanner and analysis software was developed by R. X. Xia. The succinyl anhydride reaction was suggested by J. Mulligan and J. Van Ness of Darwin Molecular Corporation. Thanks to S. Theologis, C. Somerville, K. Yamamoto, and members of the laboratories of R.W.D. and P.O.B. for critical comments. Supported by the Howard Hughes Medical Institute and by grants from NIH (R21HG00450) (P.O.B.) and R37AG00198 (R.W.D.) and from NSF (MCB9106011) (R.W.D.) and an NSF graduate fellowship (D.S.). P.O.B. is an assistant investigator of the Howard Hughes Medical Institute.

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Gene Therapy in Peripheral Blood Lymphocytes and Bone Marrow for ADA⁻ Immunodeficient Patients

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Adenosine deaminase (ADA) deficiency results in severe combined immunodeficiency, the first genetic disorder treated by gene therapy. Two different retroviral vectors were used to transfer ex vivo the human ADA minigene into bone marrow cells and peripheral blood lymphocytes from two patients undergoing exogenous enzyme replacement therapy. After 2 years of treatment, long-term survival of T and B lymphocytes, marrow cells, and granulocytes expressing the transferred ADA gene was demonstrated and resulted in normalization of the immune repertoire and restoration of cellular and humoral immunity. After discontinuation of treatment, T lymphocytes, derived from transduced peripheral blood lymphocytes, were progressively replaced by marrow-derived T cells in both patients. These results indicate successful gene transfer into long-lasting progenitor cells, producing a functional multilineage progeny.

Severe combined immunodeficiency associated with inherited deficiency of ADA (1) is usually fatal unless affected children are kept in protective isolation or the immune system is reconstituted by bone marrow transplantation from a human leukocyte antigen (HLA)-identical sibling donor (2). This is the therapy of choice, although it is available only for a minority of patients. In recent years, other forms of therapy have been developed, including transplants from haploidentical donors (3, 4), exogenous enzyme replacement (5), and somatic-cell gene therapy (6-9).

We previously reported a preclinical model in which ADA gene transfer and expression

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successfully restored immune functions in human ADA-deficient (ADA⁻) peripheral blood lymphocytes (PBLs) in immunodeficient mice *in vivo* (10, 11). On the basis of these preclinical results, the clinical application of gene therapy for the treatment of ADA⁻ SCID (severe combined immunodeficiency disease) patients who previously failed exogenous enzyme replacement therapy was approved by our Institutional Ethical Committees and by the Italian National Committee for Bioethics (12). In addition to evaluating the safety and efficacy of the gene therapy procedure, the aim of the study was to define the relative role of PBLs and hematopoietic stem cells in the long-term reconstitution of immune functions after retroviral vector-mediated ADA gene transfer. For this purpose, two structurally identical vectors expressing the human ADA complementary DNA (cDNA), distinguishable by the presence of alternative restriction sites in a nonfunctional region of the viral long-terminal repeat (LTR), were used to transduce PBLs and bone marrow (BM) cells independently. This procedure allowed identification of the origin of